Remarks

Claims 35-52 are pending. Claims 1-34 were previously cancelled without prejudice to or disclaimer of the underlying subject matter. Claim 50 has been amended. Support for the amendments can be found throughout the specification and claims as originally filed, for example on page 10, line 10 through page 12, line 1, and in the original claims. No new matter enters by this amendment.

I. Withdrawn Rejections

Applicants acknowledge and thank the Examiner for indicating that the rejection of "claim 50, under 35 U.S.C. 112, first paragraph for failing to comply with the written description requirement for new matter ... is withdrawn." Office Action at page 2.

Applicants also acknowledge and thank the Examiner for indicating that the "rejection of claims 35-37, 41-42, 45-49 under 35 U.S.C. ... is withdrawn." *Id.*

II. Rejection under 35 U.S.C. § 112 - Written Description

Claim 50 is newly rejected under 35 U.S.C. § 112, first paragraph for allegedly "[containing] subject matter, which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention." Office Action at page 3. Applicants respectfully traverse this rejection.

More particularly, the Examiner argues that "the recitation of 'hybridizes under stringent hybridization conditions' allows for polynucleotides with substantial variation with regard to [the] 3' end of the P. sativum rbcS E9 gene." Office Action at page 3.

The Examiner acknowledges that "the specification teaches examples of appropriate stringency hybridization conditions," but argues that the specification "fails to set forth a clear definition for the term 'stringent conditions' and thus the metes and bounds of the conditions encompassed allow for polynucleotides with substantial variation with regard to the 3' untranslated sequence of the 3' end of the P. sativum rbcS E9 gene." *Id.* The Examiner concludes that "[t]he instant claim is drawn to undisclosed sequences encoding modification that have not been contemplated" and therefore "[t]he specification provides insufficient written description to support the genus encompasses by the claim." *Id.* at page 4. Applicants respectfully disagree.

The specification provides sufficient disclosure such that a person of ordinary skill in the art would, after reading the present specification, understand that Applicants had possession of the claimed invention. For example, the specification describes gene sequences, including the 3' untranslated region, corresponding sequences, preferred sequences, and so forth of the *Pisum sativum* rbcS E9 gene (*see, e.g.,* specification at page 26, line 1 through page 28, line 14; in the Sequence Listing; and in the claims as originally filed). The specification also describes appropriate hybridization conditions (*see, e.g.,* specification at page 12, line 12 through page 13, line 18); oligonucleotides and primers for obtaining oligonucleotides (*see, e.g.*, specification at page 9, line 22 through page 10, line 24 and in the sequence listing); oligonucleotides that hybridize to 3' untranslated regions (*see, e.g.* specification at page 21, line 17 through page 22, line 4 and in the sequence listing); and expression detection and quantitation methods (*see, e.g.*, specification at page 28, line 15 through page 37, line 9). Despite the numerous

variations described for the nucleic acid molecules in the present specification, the Examiner argues that "[w]ith the exception of SEQ ID NOS: 2, 7-9, and 28, the skilled artisan cannot envision the detailed chemical structure of the encompassed polynucleotides, regardless of the complexity or simplicity of the method of isolation." Office Action at page 5.

The purpose of the written description requirement is to ensure that the inventor had possession of the claimed subject matter, *i.e.*, to ensure that the inventor actually invented what is claimed. *Gentry Gallery Inc. v. Berkline Corp.*, 134 F.3d 1473, 1479, 45 U.S.P.Q.2d 1498, 1503 (Fed. Cir. 1998); *Lockwood v. American Airlines*, 107 F.3d 1565, 1572, 41 U.S.P.Q.2d 1961, 1966 (Fed. Cir. 1997); *In re Alton*, 76 F.3d 1168, 1172, 37 U.S.P.Q.2d 1578, 1581 (Fed. Cir. 1996). In accordance with this purpose, Applicants need not "describe," in the sense of Section 112, all things that are encompassed by the claims. To contend otherwise would contradict established jurisprudence, which teaches that a patent may be infringed by technology developed after a patent issues. *United States Steel Corp. v. Phillips Petroleum Co.*, 865 F.2d 1247, 1251, 9 U.S.P.Q.2d 1461, 1464 (Fed. Cir. 1989). A related, and equally well-established principle of patent law is that claims "may be broader than the specific embodiment disclosed in a specification." *Ralston Purina Co. v. Far-mor-Co*, 772 F.2d 1570, 1575, 227 U.S.P.Q. 177, 179 (Fed. Cir. 1985), *quoting In re Rasmussen*, 650 F.2d 1212, 1215, 211 U.S.P.Q. 323, 326 (C.C.P.A. 1981). Thus, simply because the nucleic acid sequences may also include sequences corresponding "to mutants, variants, and homologs of the 3' end of the *Pisum*

sativum rbcS E9 gene" does not require that Applicants describe each and every one of these molecules.

In this regard, the written description requirement can be met by "show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics...*i.e.,* complete or partial structure, other physical and or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics." *Enzo Biochem, Inc. v. Gen-Probe Inc.,* 323 F.3d 956, 964 (Fed. Cir. 2002). (quoting from Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112, ¶ 1 "Written Description" Requirement, 66 Fed. Reg. 1099, 1106 (Jan. 5, 2001)). Applicants have satisfied that test for written description. For example, Applicants have disclosed a structural feature, the nucleotide sequence of SEQ ID NO: 2, as well as primers and probes corresponding to the *P. sativum* rbcS E9 3' untranslated region. This feature provides a basis for each and every nucleic acid molecule in the claimed genus. Moreover, it distinguishes the members of the claimed genus from non-members.

The Examiner further alleges that "[w]hile the specification teaches examples of appropriate stringency hybridization conditions (page 13, lines 9-13), it fails to set forth a clear definition for the term 'stringent conditions' and thus the metes and bounds of the conditions encompassed allow for polynucleotides with substantial variation with regard to the 3' untranslated sequence of the 3' end of the P. sativum rbcS E9 gene." Office Action at page 3. The Examiner again alleges that the "[e]ven stringent hybridization would tolerate mismatches and result in sequences that correspond to mutants, variants,

and homologs of the 3' end of the *Pisum sativum* rbcS E9 gene which is not disclosed in the specification." *Id.* The Examiner concludes that the "specification only discloses a selected number of species of the genus; i.e. SEQ ID NO 2 (SEQ ID 7-9 and 28, which are part of SEQ ID NO 2), which is insufficient to put one of ordinary skill in the art in possession of all attributes and features of all species within the genus." *Id.* at page 4. As discussed above, the skilled artisan is knowledgeable of the *P. sativum* rbcS E9 gene structure. A specification cannot fail to meet the written description requirement simply because it does "not reiterate the structure or formula or chemical name" for known nucleotide sequences. *Capon v. Eshhar*, 418 F.3d 1349 (Fed. Cir. 2005).

In light of the detailed disclosure of the present application, one skilled in the art, after reading the present specification, would clearly know if a nucleic acid molecule contains one of the recited nucleotide sequences. Thus, pending claim 50 is supported by an adequate written description pursuant to the requirements of 35 U.S.C. § 112. Reconsideration and withdrawal are respectfully requested.

III. Rejection under 35 U.S.C. §102

Claim 50 is newly rejected under 35 U.S.C. § 102(b) as allegedly anticipated by 1997 Biochemicals Catalog of Boehringer Mannheim. Office Action at page 8.

Claims 35-37, 41-42, 45-46, and 48-50 remain rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Fleming, *et al.*, *Plant Journal*, 1996, 10(4): 745-754.

Claims 35, 41, 47, and 49 also remain rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Hamilton, *et al. Gene*, 1997.

A. 1997 Biochemicals Catalog of Boehringer Mannheim

Claim 50 has been rejected under 35 U.S.C. 102(b) as allegedly anticipated by the 1997 Biochemicals Catalog of Boehringer Mannheim. Office Action at page 8.

The Examiner asserts that "Boehringer Mannheim teach a hexanucleotide mixture of all possible sequences for random primed DNA labelling." *Id.* The Examiner argues that the "hexanucleotide mixture is a kit that would detect a transgenic nucleic acid molecule that would hybridize to the 3' untranslated sequence of a 3' end of the P. sativum rbcS E9 gene and comprises one primer pair and labeled probe since it contains all possible sequences of hexamers, which would encompass at least one primer pair and labeled probe (a hexamer that is partially complementary to the sequence of the 3' untranslated sequence of a 3' end of the P. sativum rbcS E9 gene with the mismatch nucleotide being the label)."

Although Applicants disagree, to facilitate prosecution, claim 50 has been amended herein to recite that the primers contain at least 15 nucleotides. Whatever else Boehringer Mannheim discloses, it does not teach or suggest a primer pair in which at least one of the primers contains at least 15 nucleotides. Absent a teaching of each and every element of the claim, the reference cited by the Examiner does not anticipate claim 50 and the rejection should be withdrawn.

Accordingly, for at least the foregoing reasons, the rejection of claim 50 under 35 U.S.C. § 102(b) is improper. Reconsideration and withdrawal of this rejection is respectfully requested.

B. Fleming *et al.*, *Plant Journal*, 1996

Claims 35-37, 41-42, 45-46, and 48-50 stand rejected under 35 U.S.C. 102(b) as allegedly anticipated by Fleming *et al.* The Examiner asserts that:

> Fleming et al. teach reverse transcription of each rbcS gene (first transgenic nucleic acid) followed by PCR (instant claim 41-42) of the cDNA from each RNA sample using a common 5' primer for the coding region and a gene-specific 3' primer for each of the 3' UTR of the genes of rbcS.

Office Action at page 9.

"It is axiomatic that for prior art to anticipate under § 102 it has to meet every element of the claimed invention." *Hybritech Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d 1367, 231 U.S.P.Q. 81 (Fed. Cir. 1986). Further, "an anticipation rejection requires a showing that each limitation of a claim must be found in a single reference, practice, or device." *In re Donohue*, 766 F.2d 531, 226 U.S.P.Q. 619 (Fed. Cir. 1985).

Initially, Applicants maintain their disagreement with the Examiner's characterization of the reference as teaching "that the nucleic acids for use in RT-PCR were transgenic nucleic acids." Office Action at page 11. However, nothing the Examiner cites to indicates that the plants analyzed by RT-PCR were transgenic. For example, the Examiner cites page 751 of Fleming as teaching "RT-PCR of RBCS gene expression in tomato, which was described in the experimental procedures as a transgenic plant containing the tomato RBCS 5' sequence." Office Action at page 11. Applicants respectfully disagree. The experimental procedures of Fleming suggests that the authors used two sources of plant material for the procedures employed - one source for use in RT-PCR and another source for GUS expression analysis. For example, the

Experimental procedures section of Fleming states that "[f]or RT-PCR and *in situ* hybridization, seedlings of *Lycopersicon esculentum* cv. Moneymaker were grown in soil...." Fleming *et al.* at page 751, column 2. However, transgenic plants were specifically indicated as the tissue source for other procedures discussed in the reference. For example, the authors indicate that "[f]or analysis of GUS expression by histochemical assay, immunocytochemistry and fluorescent imaging, *transgenic* F1 seeds were germinated and grown...." *Id.* (emphasis added). The Examiner argues, however, that "Fleming et al. teach RT-PCR of RBCS gene expression in tomato, which was described in the experimental procedures as a transgenic plant containing the tomato RBCS 5' sequence (see page 751, RBCS gene expression in developmentally controlled leaf initiation)." Office Action at page 11. Again, as discussed above, the experimental procedures section provides that plant material for RT-PCR and *in situ* hybridization was obtained from *Lycopersicon esculentum* cv Moneymaker. *See*, Fleming *et al.* at page 751, first paragraph under the heading "Plant Material and tissue culture." Nothing in the experimental procedures section suggests that transgenic plants were also the source of plant material for RT-PCR and as such are not directed to detecting expression of a first transgenic nucleic acid molecule.

Moreover, Fleming *et al.* nowhere mentions hybridization to a second transgenic to indicate the expression of a first transgenic nucleic acid molecule. As the Examiner acknowledges, Fleming discusses the use of a "common 5' primer in the coding region" of the rbcS gene. Fleming, *et al.*, at page 752, Figure 5. Accordingly, the resulting amplification product includes sequence from the coding sequence of rbcS, or the first

transgenic nucleic acid molecule, and therefore is not designed to hybridize to the second transgenic nucleic acid molecule. Hybridization with the resulting amplification product from the first nucleic acid would hybridize to itself. As such, the method discussed in Fleming *et al.* is not used as a surrogate indicator for a first transgenic nucleic acid molecule.

The Examiner argues in the alternative that "Fleming et al. teach a method of semi-quantitative RT-PCR analysis of gene-specific rbcS transcript levels." Office Action at page 10. The Examiner argues that the cited reference teaches "that rbcS gene-specific transcript levels are expressed relative to the signal obtained using the RPL2 primers at corresponding sample dilutions (detecting expression of second transgenic nucleic acid which indicates expression of first transgenic nucleic acid)." *Id.* Applicants respectfully disagree with the Examiner's characterization of the reference.

Contrary to the Examiner's assertion that the "detecting expression of second transgenic nucleic acid which indicates expression of [the] first transgenic nucleic acid," the RPL2 amplification product is used as an internal control to determine the relative level of expression of the native rbcS gene. As discussed above, Fleming *et al.* disclose that the plant material used for RT-PCR analysis was obtained from *Lycopersicon esculentum* cv Moneymaker. Nothing the Examiner points to suggests that these plants were "transgenic." For example, unlike the plants material for RT-PCR, Fleming *et al.* specifically states that the plant material for GUS analysis was grown from "transgenic F1 seeds." Fleming at page 751 (emphasis added). The Examiner has pointed to no evidence to support that either the rbcS or RPL2 sequence was transgenic.

In summary, whatever else Fleming *et al.* teaches, it does not disclose a method to detect the expression of a first transgenic nucleic acid molecule in sample comprising providing a complementary DNA of a mRNA transcribed from a second transgenic nucleic acid molecule. Absent a teaching of each and every element of the claims, the reference cited by the Examiner does not anticipate claims 35-37, 41-42, 45-46, and 48-50 and the rejection should be withdrawn.

Accordingly, for at least the foregoing reasons, the rejection of claims 35-37, 41-42, 45-46, and 48-50 under 35 U.S.C. § 102(b) is improper. Reconsideration and withdrawal of this rejection is respectfully requested.

C. Hamilton *et al.*, *Gene*, 1997

Claims 35, 40, 41, 47 and 49 remain rejected under 35 U.S.C. 102(b) as allegedly being anticipated by Hamilton *et al.* In support of this rejection, the Examiner asserts that:

> Hamilton demonstrates the expression of transgenes in a BIBAC vector (p. 113, 2nd column, 3rd paragraph), wherein a successful transfection into the host plant is determined based upon the following transgenic nucleic acids: *sacB* gene, GUS-NPTII gene (beta-glucuronidase – neomycin phosphotransferase II), and the HYP gene (hygromycin phosphotransferase). In one example, the first transgenic nucleic acid is the *sacB* gene and the second transgenic acid is the GUS-NPTII and/or HYG gene:
>
> > Potential transgenic plants were initially tested by PCR using primers to the GUS-NPTII and HYG [...]. [...] Plants that tested positive for the BIBAC T-DNA by PCR [*thereby amplification, claim 35 step ii, and claim 41*] were all verified by Southern analysis [*thereby hybridization, claim 35 step iii, and claim 49*] using a NPTII specific probe. (p. 113, 1st column, 3rd paragraph) (see also figure 3).

Office Action at page 13.

This rejection is respectfully traversed for at least the reasons which follow. As previously set forth, it is well established that to anticipate a claim, a reference must disclose every element of the claim. *Verdegaal Bros. v. Union Co. of California*, 2 U.S.P.Q.2d 1051, 1053 (Fed. Cir. 1987). The identical invention must be shown in complete detail as is contained in the claim. *Richardson v. Suzuki Motor Co.*, 9 U.S.P.Q.2d 1913, 1920 (Fed. Cir. 1989).

Applicant respectfully submits that the Hamilton *et al.* disclosure does not include all of the limitations of the present claims. Whatever else Hamilton *et al.* teaches, it does not disclose a method to detect the expression of a first nucleic acid molecule in sample. Applicants maintain their disagreement with the Examiner's characterization of the reference. In particular, the Examiner asserts that "Hamilton teaches that plants that tested positive for BIBAC T-DNA by PCR were verified by southern analysis using a NPTII probe and southern analysis is a technique that detects expression of a sequence by hybridization of the probe." Office Action at page 13. The Examiner argues that "one of skill in the art would recognize that the southern analysis step of Hamilton inherently teaches hybridization of the nucleic acid molecule which would indicate expression of the nucleic acid molecule." *Id.* at page 14.

The Examiner has provided no support for the proposition that Southern Hybridization would necessarily detect the expression of a nucleic acid molecule. The passages quoted by the Examiner recite that BIBAC T-DNA was hybridized with a GUS-NPTII-specific probe or a HYG-specific probe. (emphasis added). The Examiner has

not provided any support for the apparent assertion that the presence of the BIBAC DNA sequence in a transgenic plant would necessarily lead to the expression of that DNA sequence or produce an mRNA. Moreover, as Sambrook *et al.* discuss, Southern Hybridization is usually employed to localize particular sequences within genomic DNA and typically involves the immobilization of genomic DNA on nitrocellulose membrane. *See,* Sambrook, *et al., Molecular Cloning, A Laboratory Manual,* vol. 2, § 9, 31-58 (2d ed., Cold Spring Harbor Laboratory Press, 1989) (submitted herewith). The *expression* of a particular nucleic acid is usually detected using Northern Hybridization or other techniques, but not Southern hybridization. *Id.* at vol. 1, § 7, p39 (submitted herewith). As such, the skilled artisan would recognize that because Southern Hybridizations involve the hybridization of a probe to DNA, it would not necessarily follow that such hybridization would indicate that the detected DNA is also expressed.

Accordingly, for at least the foregoing reasons, the rejection of claims 35, 36, 40-42 and 44-47 under 35 U.S.C. § 102(a) is improper. Reconsideration and withdrawal of this rejection is respectfully requested.

IV. Rejection under 35 U.S.C. § 103

Claims 35-52 remain rejected under 35 U.S.C. § 103(a) as allegedly being un-patentable over Hunt *et al.* (*DNA*, 1988), taken in combination with Freeman *et al.* (*BioTechniques*, 1999). This rejection is respectfully traversed for at least the reasons which follow.

To establish a *prima facie* case of obviousness, the prior art reference (or references when combined) must teach or suggest all of the claim limitations. There

must be some suggestion or motivation, either in the references themselves or in the knowledge generally available to one of ordinary skill in the art, to modify the reference or to combine reference teachings. The teaching or suggestion to make the claimed combination must be found in the prior art, and not be based on applicant's disclosure. *See* M.P.E.P. §§2143.01 and 2143.03.

In a proper obviousness determination, the changes from the prior art must be evaluated in terms of the whole invention, including whether the prior art provides any teaching or suggestion to one of ordinary skill in the art to make the changes that would produce the claimed invention. *See In re Chu,* 36 USPQ2d 1089, 1094 (Fed. Cir. 1995). This includes what could be characterized as simple changes. *See, e.g., In re Gordon,* 221 USPQ 1125, 1127 (Fed. Cir. 1984) (Although a prior art device could have been turned upside down, that did not make the modification obvious unless the prior art fairly suggested the desirability of turning the device upside down.).

Only when the prior art teaches or suggests the claimed invention does the burden fall on the applicant to rebut that *prima facie* case. *See In re Dillon,* 16 USPQ2d 1897, 1901 (Fed. Cir. 1990) (in banc), *cert. denied,* 500 U.S. 904 (1991). However, a *prima facie* case of obviousness may be rebutted by showing that the art, in any material respect, teaches away from the claimed invention.

The Office has not shown that the cited references teach or suggest the claimed invention. The Examiner argues that Hunt *et al.* discloses "the transformation of a tobacco plant with a plasmid carrying the 3' noncoding strand of the pea rbcS-E9 3' region (claims 37, 38) which aligns 99.5% with SEQ ID NO: 2 (a 637 bp sequence) from residue

1-633 (claim 39), and a desired transgene pAH10 (figure 2A)." Office Action at page 16. The Office acknowledges that Hunt *et al.*, however, "does not teach the amplification by PCR or RT-PCR, quantitative and competitive RT-PCR, the primers utilized for the amplification as required by claims 36, 41, 42, 47, 48 and 50." *Id.* at page 17.

The Examiner argues that "Freeman teaches the benefits of PCR, specifically utilizing quantitative RT-PCR, both competitive and non-competitive (pp. 116-117) to *quantify* mRNA (claims 36, 41, 42)." *Id.* (emphasis added). Applicants respectfully submit that the cited references do not render the present independent claims obvious, since the claims are not taught nor suggested by the cited references. The cited references do not disclose or suggest a method to detect the expression of a first transgenic nucleic acid molecule in a sample comprising amplifying a complementary DNA from an mRNA from a second transgenic nucleic acid molecule and hybridizing the cDNA with at least one oligonucleotide designed to hybridize to the second transgenic nucleic acid molecule where hybridizing indicates the expression of the first transgenic nucleic acid molecule in a sample.

The Examiner has stated that "it would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to improve the detection method of Hunt et al and further modify the mRNA expression analysis to utilize quantitative RT-PCR which includes amplification along with primers and probes designed for quantitative RT-PCR as per the teachings of Freeman et al. because Freeman teaches that quantitative RT-PCR provides increased sensitivity in mRNA detection." Office Action at page 18.

Initially, Applicants respectfully disagree with the Examiner's characterization of the art. By way of example, the Examiner asserts that "it would have been prima facie obvious ... to improve the detection method of Hunt, *et al*...." *Id.* In this regard, Applicants note that nowhere does Hunt *et al.* disclose or suggest a method for detecting the expression of a first transgenic nucleic acid molecule. As previously discussed, Hunt, *et al.* faced the problem of identifying sequence requirements for the polyadenylation of mRNAs in plants. The cited reference shows "that the 3' region of the pea *rbcS*-E9 gene has a number of discrete, cryptic polyadenylation sites located downstream from the previously-determined poly(A) sites of this gene." Hunt, *et al.*, at page 329, second column, last sentence. The Examiner has not cited any support for the proposition that the methods discussed in Hunt were not sufficient to solve the problem faced in Hunt and would therefore require improvement. As such, it is respectfully submitted that the Examiner's conclusion of obviousness is based on improper reasoning and a misinterpretation of the art.

Moreover, the modification of Hunt, *et al.* proposed by the Examiner would render the reference unsatisfactory for its intended purpose. *See,* MPEP 2143.01. Hunt *et al.* discusses that "[t]he sequence requirements for the polyadenylation of mRNAs in plant have not been carefully studied." Hunt et al. page 329, Second column. S1 nuclease protection analysis was performed to identify 3' ends in the rbcS 3' region. *Id.* at page 332, paragraph spanning columns 1 and 2. The Examiner has not cited any language that modifying Hunt *et al.* as suggested by the Examiner to use RT-PCR would identify the sequences of 3' ends responsible for the polyadenylation of mRNAs. Rather,

Freeman *et al.* generally discuss RT-PCR for the quantification of steady-state mRNA levels. Hunt *et al.* discusses the identification of a number of discrete, cryptic polyadenylation sites in the rbcS 3' sequence. The Examiner argues that "[a]n ordinary artisan would have been motivated to use quantitative RT-PCR amplification instead of the S1 nuclease assay in the detection method of Hunt et al, for increased specificity and decreased background as per the teachings of Freeman et al." Office Action at pages 18-19. The Examiner has not provided any support that Freeman and Hunt could be combined to analyze the rbcS 3' sequence for polyadenylation sequences, or that the S1 nuclease assay of Hunt could be combined with Freeman to reach the instant claims.

Even assuming *arguendo* that the combination is proper, the combination does not render the claimed invention obvious. Whatever else Hunt *et al.* and Freeman *et al.* disclose, the do not teach or suggest a method to detect the expression of a first transgenic nucleic acid molecule in a sample by hybridizing a complementary DNA of mRNA transcribed from a second transgenic nucleic acid molecule with at least one oligonucleotide designed to hybridize to the second transgenic nucleic acid molecule where the hybridization indicates the expression of the first transgenic nucleic acid molecule in the sample. The Examiner has not pointed to any specific suggestion in any of the cited references to reach the presently claimed invention. It is impermissible hindsight to find it obvious for one skilled in the art to combine the cited references to reach the invention in the present application absent some suggestion or motivation in the cited references. Therefore, it would not be obvious to one skilled in the art, from reading Hunt *et al.* and Freeman *et al.* that one could obtain the methods of the present invention.

Moreover, the skilled artisan would not turn to Hunt *et al.* to solve the problem of detecting the expression of a first transgenic nucleic acid molecule. "In order to rely on a reference as a basis for rejection of an applicant's invention, the reference must either be in the field of applicant's endeavor or, if not, then be reasonably pertinent to the particular problem with which the inventor was concerned." *In re Oetiker*, 977 F.2d 1443, 1446, 24 USPQ2d 1443, 1445 (Fed. Cir. 1992). *See also In re Deminski*, 796 F.2d 436, 230 USPQ 313 (Fed. Cir. 1986); *In re Clay*, 966 F.2d 656, 23 USPQ2d 1058 (Fed. Cir. 1992). Applicants maintain that Hunt *et al.* is not analogous art. The Hunt *et al.* reference is not in the Applicant's field of endeavor. The Hunt *et al.* reference describes the identification of "a number of discrete, cryptic polyadenylation sites located downstream from the previously-determined poly(A) sites of" the 3' region of the pea *rbcS*-E9 gene. This is a different field of endeavor from the methods for detecting the expression of a first transgenic nucleic acid molecule in a sample by hybridizing a complementary DNA of mRNA transcribed from a second transgenic nucleic acid molecule with at least one oligonucleotide designed to hybridize to the second transgenic nucleic acid molecule where the hybridization indicates the expression of the first transgenic nucleic acid molecule in the sample.

In sum, the Examiner's conclusion of obviousness is based on improper hindsight reasoning. "Impermissible hindsight must be avoided and the legal conclusion must be reached on the basis of the facts gleaned from the prior art." M.P.E.P. § 2142 at 2100-124. No suggestion to modify the cited references has been found in the cited references or pointed out to Applicant from the general knowledge of one of ordinary skill in the art.

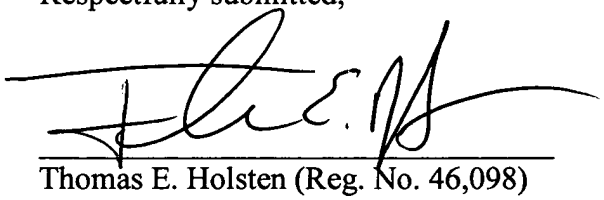
In addition, no indication for Hunt *et al.* teaching the claimed method is provided. For at least these reasons, the Applicant respectfully submits that the Examiner has failed to establish a *prima facie* case of obviousness, as required by 35 U.S.C. § 103.

Accordingly, for at least the foregoing reasons, the rejection of claims 35-52 under 35 U.S.C. § 103 is improper. Reconsideration and withdrawal of this rejection are respectfully requested.

Conclusion

In view of the foregoing remarks, Applicants respectfully submit that the present application is now in condition for allowance, and notice of such is respectfully requested. The Examiner is encouraged to contact the undersigned should any additional information be necessary for allowance.

Respectfully submitted,



Thomas E. Holsten (Reg. No. 46,098)
David R. Marsh (Reg. No. 41,408)

ARNOLD & PORTER LLP
555 Twelfth Street, N.W.
Washington, DC 20004-1206
Tel.: 202.942.5000
Fax: 202.942.5999

Filed: May 23, 2006

Of counsel:
Lawrence M. Lavin, Jr. (Reg. No. 30,768)
Thomas E. Kelley (Reg. No. 29,938)
Monsanto Company

Correspondence Address:
Monsanto Company
Patent Department, E2NA
800 N. Lindbergh Boulevard
St. Louis, Missouri 63167
Tel: 314-694-1000
Fax: 314-694-9009